

FIG. 1

```

1      GTCCCTTCCACCATGCACTCGCTGGGCTTCTTCTCTGTGGCGTCTCTGCTCGCCGCTG
-----+-----+-----+-----+-----+-----+-----+-----+
C      CAGGAAGGTGCTACGTGAGCGCACC CGAAGAAGACACCCGACAAGAGACGAGCCGCCAC
      M H S L G F F S V A C S L L A A A -
61     CGCTGCTCCCGGCTCTCGGAGGCGCCGCGCCGCCGCTTCGAGTCCGACTCG
-----+-----+-----+-----+-----+-----+-----+
C      CGGACGAGGCCCGAGGACGCTCCGCGCGCGCGCGCGGAGCTCAGGCTGAGC
      L L P G P R E A P A A A A F E S G L D -
121    ACCTCTCGGACCGCGAGCCCGGCGCGGCGGAGGCCACGGCTTATGCAAGCAAGATCTGG
-----+-----+-----+-----+-----+-----+-----+
C      TGGAGAGCCTGCGCCTCGGGCTGCGCCGCTCCGGTGCCGAATACGTTCTTAGACC
      L S D A E P D A G E A T A Y A S K D L E -
181    AGGAGCAGTTACGGTCTGTGTCCAGTGTAGATGAATCATGACTGACTCTACCCAGAAT
-----+-----+-----+-----+-----+-----+-----+
C      TCCTCGTCAATGCCAGACACAGGTCACATCTACTTGAGTACTGACATGAGATGGTCTTA
      E Q L R S V S S V D E L M T V L Y P E Y -
241    ATTGAAATGTACAAGTGTCAAGCTAAGGAAAGAGGCTGCCACATAACAGAGAACAGG
-----+-----+-----+-----+-----+-----+-----+
C      TAACCTTTTACATGTTACACAGTCGATTCCTTTCCTCGACCGTGTATTGTCTCTGTCC
      W K M Y K C Q L R K G G W Q H N R E Q A -
300    CCAACCTCAACTCAGGACAGAGAGACTATAAATTTGCTGCAGCACATTATAATACAG

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MATCH WITH FIG. 1B

# Q&A: What's New in the 2015 Edition of the Code of Ethics?

FIG. 1

[illegible]

GGTTGAGCTTGAGTTCCCTGCTCTCTGATATTTTAAACGACGTCGTGTAATATTATGTC  
N L N S R T E E T I K F A A A H Y N T E -

AGATCTTGAAGAATTTGATAATGAGTGGAGAAAGACTCAATGCATGCCACGGGAGGT 420

I L K S I D N E W R K T Q C M P R E V C -  
 TCTAGAACTTTTCATTAATACTATTACTCACCCTCTTTCTGAGTTACGTAACGTCCTCCACA

[illegible]

CATATCTACACCCCTTCTCTCAAACTCAGCGCTGTTGCTGAAGAAATTGAGGTACAC  
I D V G K E ' F G V A T N T F F K P P C V -

TGTCCGCTACAGATGCGGGCTTCTCCAATAGTGAGGGCTGCAGTGCATGAACCA  
 -----+-----+-----+-----+-----+-----+-----+ 540

ACAGGCAGATGCTTACACCCCCAACGACGTTATCACTCCCGACGTCACGTA CTGTGCT  
S V Y R C G G C C N S E G L O C M N T S -

GCACGAGCTACC TCAGCAGA GCGTATT TGAATTA CAGTGCC CTCTCTCA AGGCCCA  
-----+-----+-----+-----+-----+-----+ 600

CGTGCCTCGATGGAGTCGTTCTGCAATAACTTTAATGTCACGGAGAGAGACTTCCGGGT  
T S Y L S K T L F E I T V P L S O G P K -

AACCGTACAATCAGTTTCCCAATCACACTTCCGCCGATGCATGCTAACTGGATG 650

TTGGTCATTGTTAGTCAAAACGGTTAGTGTGAAGACGGCTACGTACAGATTTCACCTAC  
P V T I S F A N H T S C B C M S K L D V -

# MATCH WITH FIG. 1C

W. G. L.

09257E = 0E0E0E0E

# MATCH WITH FIG. 1C FIG. 1D

C V C K N K L F P S Q C G A N R E F D E N -

1021 ACACATGCCAGTGTGTATGTAAGAACCCTGCCCAAGAATCAACCCCTAATCCTGAA + 1080

C TGTGTACGGTCACACATACATTTTCTTGGACGGGCTTTAGTTGGGATTTAGACCTT  
T C Q C V C K R T C P R N Q P L N P G K -

1081 AATGTGCTGTGAATGTACAGAAAGTCCACAGAAATGCTTGTAAAGAAGAAGTTC + 1140

C TTACACGGACACTTACATGTCTTTACAGGTGTCTTTACGAACAATTTCTTCAAG  
C A C E C T E S P Q K C L L K G K K F H -

1141 ACCACCAACATGCAGCTGTACAGACGGCCATGTACGAACCGCCAGAAGCTTGTGAGC + 1200

C TGGTGGTTTGTACGTGACAATGTCTGCCGTACATGCTTGGCGTCTTCGAACACTCG  
H Q T C S C Y R R P C T N R Q K A C E P -

1201 CAGGATTTTCATATAGTGAAGAAGTGTGTGTCCTTCATATTTGCCAAAGACCAC + 1260

C GTCCTAAGAAGTATATCATTCTTCACACAGCAACAGGAAGTATAACCGTTTCTGCTG  
G F S Y S E E V C R C V P S Y W Q R P Q -

AAATGAGCTAAGATTGTACTGTCTTCCAGTTCATCGATTCTTCTATTATGAAAACTGTGT

MATCH WITH FIG. 1E

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Fig. 1

○

1381

1441

1501

1561

1621

1 CGAGCCACGGCTTATGCAAGCAAGATCTGGAGGACGATTACGGTCTGTGCCAGTGT  
-----+-----+-----+-----+-----+-----+-----+  
71 AGATGAACCTCATGACTGTACTCTACCCAGAATATTGAAAATGTACAGTGTCAAGCTAAG  
-----+-----+-----+-----+-----+-----+-----+  
M T V L Y P E Y W K M Y K C Q L R  
-----+-----+-----+-----+-----+-----+-----+  
121 GAAAGGAGCGCTGGCAACATAACAGAGAACAGGCCAACCCTCAACTCAAGGACAGAGAGAC  
-----+-----+-----+-----+-----+-----+-----+  
K G G W Q H N R E Q A N L N S R T E E T  
-----+-----+-----+-----+-----+-----+-----+  
181 TATAAAATTGTGCTGCAGCACATTATAATACAGAGATCTTGAAAAGTATTGATAATGAGTC  
-----+-----+-----+-----+-----+-----+-----+  
I K F A A A H Y N T E I L K S I D N E W  
-----+-----+-----+-----+-----+-----+-----+  
241 GAGAAAGACTCAATGCATGCCACGGGAGGTGTATAGATGTGGGAAGGAGTTTGAGT  
-----+-----+-----+-----+-----+-----+-----+  
R K T Q C M P R E V C I D V G K E F G V  
-----+-----+-----+-----+-----+-----+-----+  
301 CGCGACAACACCTTCTTTAAACCTCCATGTGTGTCCGCTACAGATGTGGGGTTCCTC  
-----+-----+-----+-----+-----+-----+-----+  
A T N T F F K P P C V S V Y R C G C C C

FIG. 2A

361 CAATAGTGAGGGCTGCAGTGCATGAACACGACGAGCTACCTCAGCAAGCGTTATT  
 -----+-----  
 N S E G L Q C M N T S T S Y L S K T L F  
 421 TGAATTTACAGTGCCCTCTCTCAAGCCCCAACCAGTAACAATCAGTTTGGCAATCA  
 -----+-----  
 E I T V P L S Q G P K P V T I S F A N H  
 481 CACTTCCCTGCCGATGCATGTCTAAACTGGATGTTTACAGACAAGTTTCATTCCATTATTAG  
 -----+-----  
 T S C R C M S K L D V Y R Q V H S I I R  
 541 ACCTTCCCTGCCAGCAACACTACCACAGTGTCAAGCAGCGAACAAGACCTGCCCAACCA  
 -----+-----  
 R S L P A T L P Q C Q A A N K T C P T N  
 601 TTACATGTGAATAATCACAATCTGCAGATGCCCTGGCTCAGGAAGATTTATGTTTCCCTC  
 -----+-----  
 Y M W N N H I C R C L A Q E D F M F S S  
 661 GGATGCTGGAGATGACTCAACAGATGATTCATGACATCTGTGACCAACAAGAGAGCT  
 -----+-----  
 D A G D D S T D G F H D I C G P N K E L

FIG.2B

721 GGATGAGAGACCTGTCAGTGTCTGTCAGAGCGGGCTTCGGCCTGCCAGCTGTGACC  
 -----+-----  
 D E E T C Q C V C R A G L R P A S C G P  
 -----+-----  
 781 CCACAAGAACTAGACAGAAACTCATGCCAGTGTGTCTGTAAACAACTCTTCCCAG  
 -----+-----  
 H K E L D R N S C Q C V C K N K L F P S  
 -----+-----  
 841 CCAATGTGGGGCCACCGAGAAATTGATGAACACATGCCAGTGTGTATGTAAAGAAC  
 -----+-----  
 Q C G A N R E F D E N T C Q C V C K R T  
 -----+-----  
 901 CTGCCCCAGAAATCAACCCCTTAATCCTGGAAATGTCCTGTGAATGTACAGAAAGTCC  
 -----+-----  
 C P R N Q P L N P G K C A C E C T E S P  
 -----+-----  
 961 ACAGAAATGCTTGTAAAGGAAGAAGTTCCACCACCAACATGCAGCTGTACAGACG  
 -----+-----  
 Q K C L L K G K K F H H Q T C S C Y R R  
 -----+-----  
 1021 GCCATGTACGAACCGCCAGAAAGCCTTGTGAGCCAGGATTTTCATATAGTGAAGAAGTGTG  
 -----+-----  
 P C T N R Q K A C E P G F S S Y S E E V C  
 -----+-----

FIG. 2C



1081 TCGTTGTGTCCTTCATATTGGCAAGACCACAATGAGCTAAGATTGTTACTGTTTCCA  
-----+-----+-----+-----+-----+-----+  
R C V P S Y W Q R P Q M S  
-----+-----+-----+-----+-----+-----+  
1141 GTTCATCGATTTTCTATTATGAAACTGTGTGCGCACAGTAGAACTGTCTGTGAACAGA  
-----+-----+-----+-----+-----+-----+  
1201 GAGACCCCTTGTGGGTCATGCTAACAAAGACAAGTCTGTCTTCCCTGAACCATGTGA  
-----+-----+-----+-----+-----+-----+  
1261 TAACTTTACAGAAATGGA CTGGAGCTCATCTGCAAAAGCCCTCTTGTAAGACTGTTTT  
-----+-----+-----+-----+-----+-----+  
1321 CTGCCAATGACCACAAGCCAGAATTTCTCTCTGTGATTTCTTTAAAGAATGACTATA  
-----+-----+-----+-----+-----+-----+  
1381 TAAATTTATTTCCACTAAAAATATTGTTCTGCAATTTTATAGCAACAATTCGT  
-----+-----+-----+-----+-----+-----+  
1441 AAAACTCAGCTGTGATCAATATTTTATATCATGCAAAATATGTTTAAATAAATGAAAA  
-----+-----+-----+-----+-----+-----+  
1501 TTGTATTATAAAAAAAAAAAAAAA  
-----+-----+-----+-----+-----+-----+

FIG. 2D

1  
50

Pdgfa .MRTIACLL LGGYLAHV AEAELPREV IERLARSQH SIRDLOLLE  
 Pdglb MNRCAW.LEL SLCCYLRLVS AEGDPIPEEL YEMLSDESR SFDDLQRLH  
 Vegf .....MNFLL SWVHSLALL LY.....  
 Vegf2 .....MTV LYPEYWKMYK CQ..... .LRKGWQH

51 100

Pdgfa IDSVGSEDST DTSIRAHGVH ATKHVPEKRP LPIRRKRSI. ....EEAVP  
 Pdglb GDP.GEEDGA ELDLNMTRSH SGELLES... .LARGRSLG SLTLAEPAMI  
 Vegf APMAE..... .GGGQ NHHEVVKFMD .VYQR.....  
 Vegf2 REQANLNSRT EETIKFAAAH YNTEILKSID NEWRK.....

101 150

Pdgfa AVCKTRTVIY EIPRSQVDPT SANFLIMPPC VEVKRCCTGCC NTSSVKCPDS  
 Pdglb AECCKTRTEVF EISRLIDRT NANFLVWPBC VEVQRCSGCC NNRNVQCRPT  
 Vegf SYCHPIETLV DIFQEYPDEI ..EYIFKPSV PLMRGCGCC NDEGLECVPT  
 Vegf2 TQCMPREVCI DVGKEFGVAT ..NTFFKPPC VSVYRCGGCC NSEGLQCMNT

151 200

Pdgfa RVHHRSVKVA KVEYVRKKPK LKEVQVRLEE HLECCAC.... AT.....  
 Pdglb QVQLRPVQVR KIEIVRKKPI FKATVTLLED HLAACK.... ETVAARPVV  
 Vegf EESNITMQIM RIK.PH..QG QHIGEMSFLO HNKCECRPKK DRARQEKKS  
 Vegf2 STSYLSKTLF EIT.VPLSQG PKPVTISFAN HTSCRCMSKL DVYRQVHSII

FIG. 3A

201

250

Pdgfa ....TSLNPD YREEDTDVR. ....  
Pdgfb RSPGGSQEQR AKTPQTRVTI RTVRVRBPX GKHKFKHTH DKTALKETLG  
Vegf RGR.....GKQKRRK KSRYSWSVY VGARCCIMPW SLPGPH...  
Vegf2 RRSIPATLPQ CQANKTCPT NYMWNHICR CLAQEDFMS SDAGDDSTDG

251

300

Pdgfa .....  
Pdgfb A.....  
Vegf ....CGP.....CSE RKHLFVQDP QTCCKSCNT  
Vegf2 FHDICGPKE IDEETCQVC RAGLRPASCX PHKEL..DR NSCQCVCKNK

301

350

Pdgfa .....  
Pdgfb .....  
Vegf ..DSRCARQ LEINERTCXC DKPRR.....  
Vegf2 LFPSQCGANR .EFDENTCQC VCKRTCPRNQ PLNPGKACX CTESPOKCLL

351

398

Pdgfa .....  
Pdgfb .....  
Vegf .....  
Vegf2 KGKPFHHQTC SCYRRPCTNR QKACEPGFSY SEEVCRCPVS YWQRPQMS

FIG. 3B

PERCENTAGE (%) OF AMINO ACID IDENTITIES BETWEEN EACH PAIR OF GENES IS SHOWN IN THE FOLLOWING TABLE				
	PDGF $\alpha$	PDGF $\beta$	VEGF	VEGF2
PDGF $\alpha$				
PDGF $\beta$	48.0			
VEGF	20.7	22.7		
VEGF2	23.5	22.4	30.0	

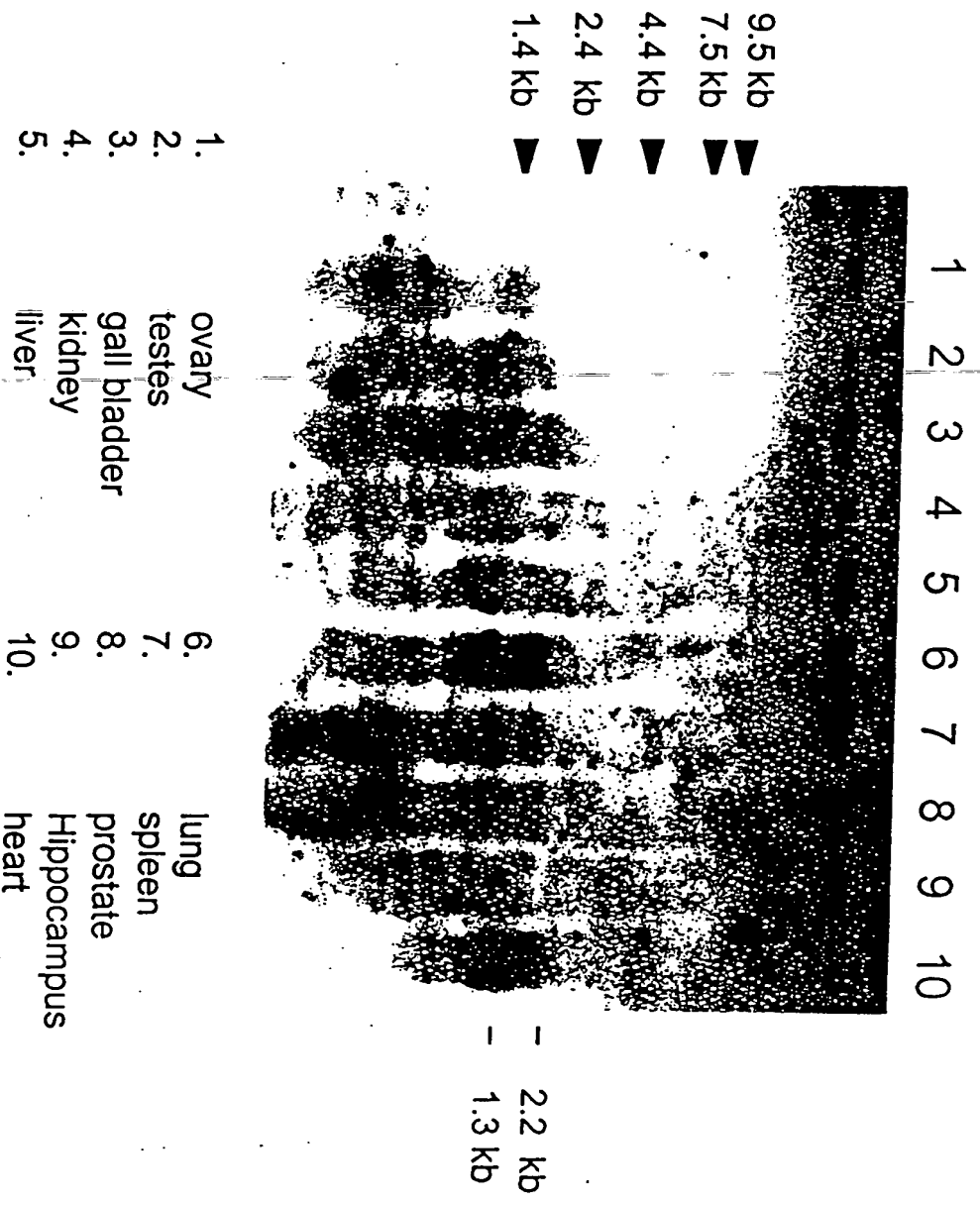
FIG. 4

Expression of VEGF2 mRNA in  
Human Breast Tumor Cells



- 1. normal breast tissue
- 2. breast tumor tissue
- 3-9. breast tumor cell lines.

FIG. 5

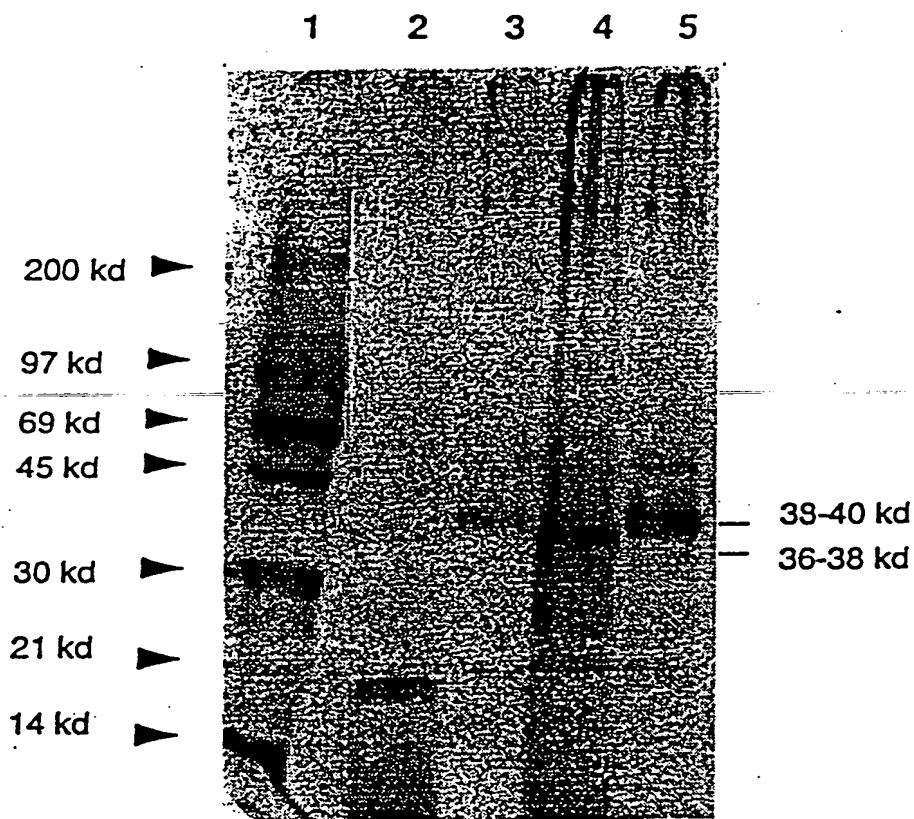


Expression of VEGF2 mRNA in human adult tissues.

FIG. 6

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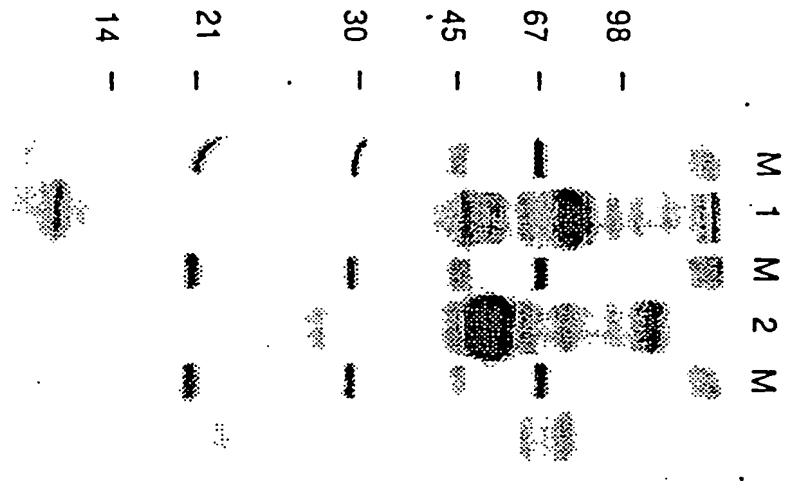
# FIG. 7



- Lane 1: 14-C and rainbow M.W. marker
- Lane 2: FGF control
- Lane 3: VEGF2 (M13-reverse & forward primers)
- Lane 4: VEGF2 (M13-reverse & VEGF-F4 primers)
- Lane 5: VEGF2 (M13-reverse & VEGF-F5 primers)

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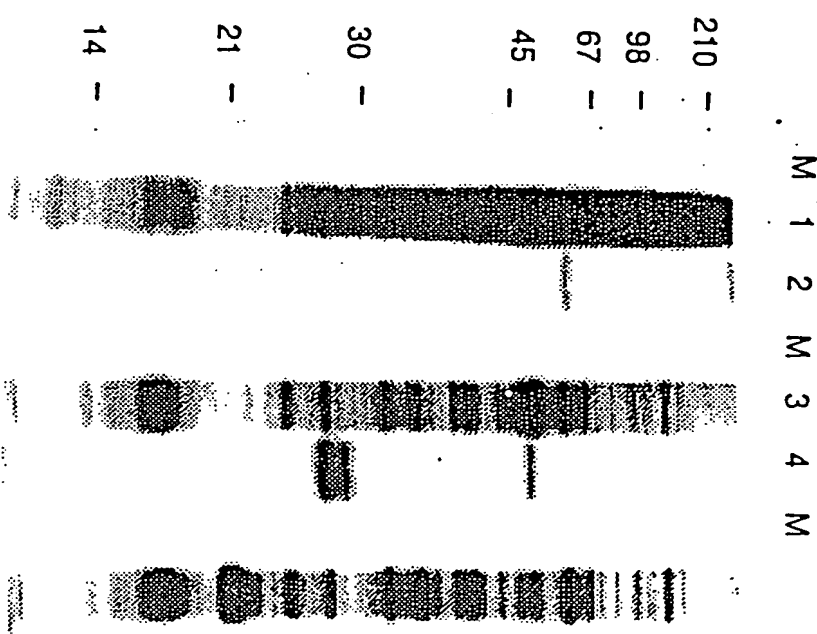
non-reducing gel



Lane M: Marker  
Lane 1: vector medium  
Lane 2: VEGF2 medium

FIG. 8A

reducing gel



Lane M: Marker  
Lane 1: vector cytoplasm  
Lane 2: vector medium  
Lane 3: VEGF2 cytoplasm  
Lane 4: VEGF2 medium

FIG. 8B



FIG. 9

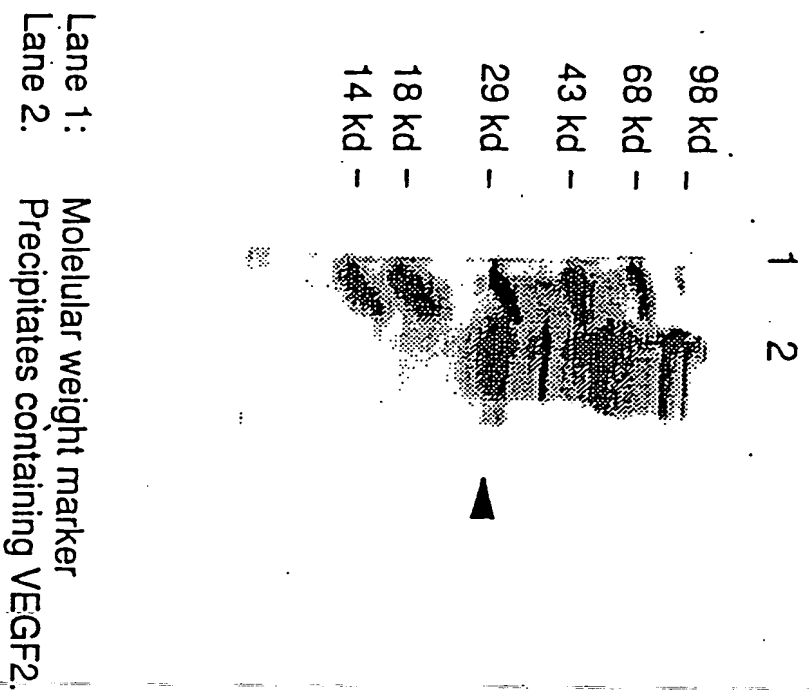


FIG. 10

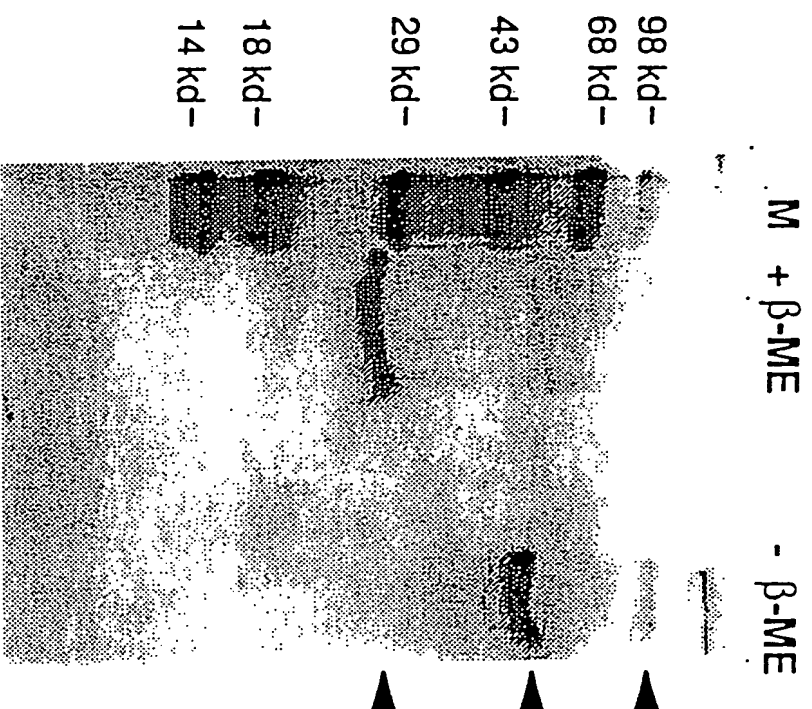
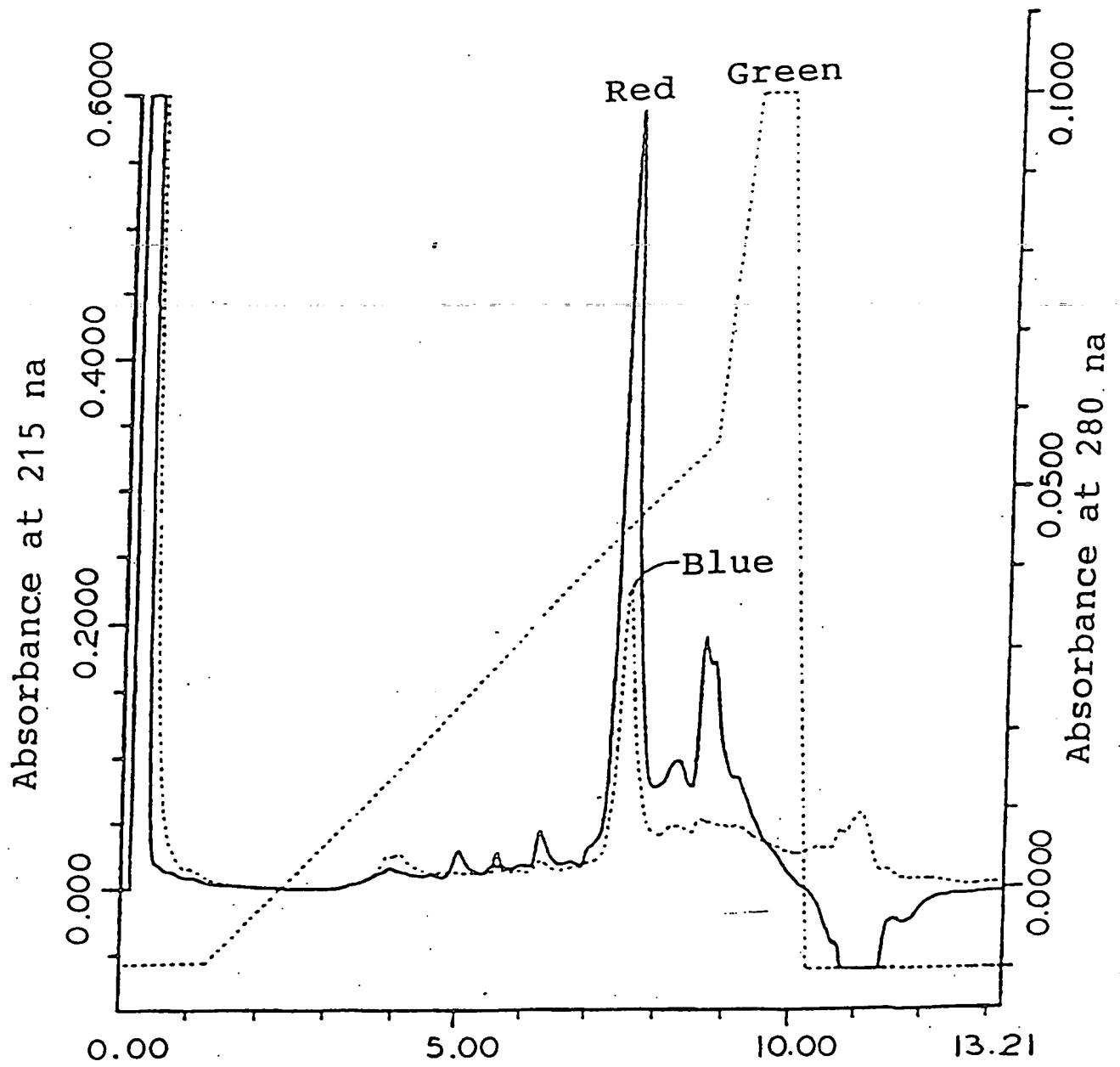


FIG. 11



0025722 025599 665220 2225260

FIG. 12

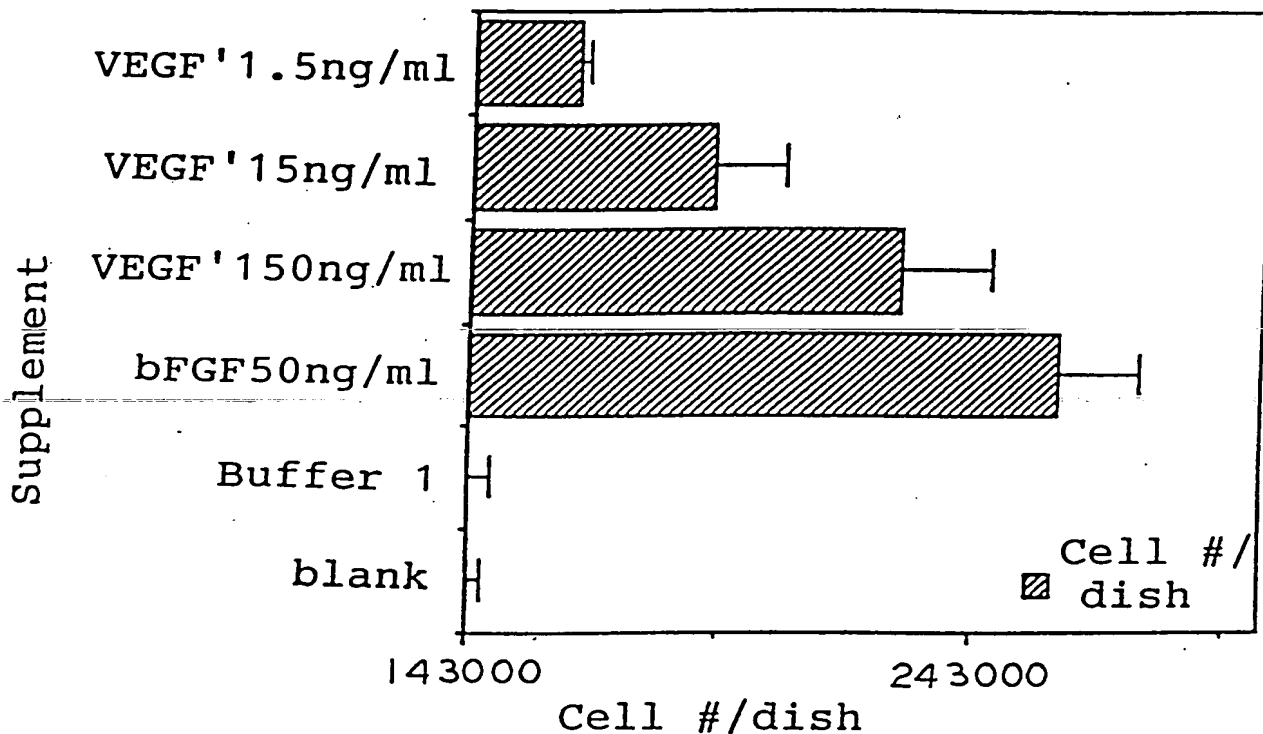


FIG. 13

